FIGURE 1

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGC**ATG**AGCGGCGGTTGGATGGCGCAGGTTGGAGCGTGGCGAACA

GGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCTGGAGGCCGCCGCGAGCCCGCTTTC

CACCCCGACCTCTGCCCAGGCCGCAGGCCCCAGCTCAGGCTCGTGCCCACCCACCAAGTTCCAGTGCCGCACCA

GTGGCTTATGCGTGCCCCTCACCTGGCGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAG

TGCAGGATTGAGCCATGTACCCAGAAAGGGCAATGCCCACCGCCCCCTGGCCTCCCCTGCCCCTGCACCGGCGT

CAGTGACTGCTCTGGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCAGGCGAGCTCC

GTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCACCCAGACTGTCCCGACTCCAGC

GACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAGGGGATGCCACAACCATGGGGCCCCCTGTGACCCT

GGAGAGTGTCACCTCTCTCAGGAATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTCG

GGAATGCCACATCCTCCTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCG

GTGCTCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCCTGGCTCCGAGCCCAGGAGCGCCTCCGCCC

ACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGACCTCGCTGCCC**TGA**GGACAAG

CACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACAGGAGGAGAGCAGTGATGCGGATGGGTACCCGG

GCACACCAGCCCTCAGAGACCTGAGTTCTTCTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCC

CTGGAGATTGAGGGTCCCTGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGA

ACTGAGGGGCTGGCCCCAGGCAGCTCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTGCCCCGT

CTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 2

MSGGWMAQVGAWRTGALGLALLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSGLCVPLTWRC

DRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKLRNCSRLACLAGELRCTLSDDCIPL

TWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVTLESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQ

SGSPTAYGVIAAAAVLSASLVTATLLLLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218, 224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 3

ACACTGGCCAAACACTCGCATCCCAGGGCGTCTCCGGCTGCTCCCATTGAGCTGTCTGCT
CGCTGTGCCCGCTGTGCCTGCTGTGCCCGCGCTGTCGCCGCTGCTACCGCGTCTGCTGGA
CGCGGGAGACGCCAGCGAGCTGGTGATTGGAGCCCTGCGGAGAGCTCAAGCGCCCAGCTC
TGCCCGAGGAGCCCAGGCTGCCCCGTGAGTCCCATAGTTGCTGCAGGAGTGGAGCCTTTC
CCTTTGCGATCGCTAAACCACC**ATG**AGCTGCGTCCTGGGTGGTGTCATCCCCTTGGGGCT
GCTGTTCCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACTCTCTTAGAGGA
GCTGCTCAGCAAATACCAGCACAACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAG
GGAGGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCA
GGCCTCCAACATGGAGTACATGACCTGGGATGACGAACTGGAGAAGTCTGCTGCAGCGTG
GGCCAGTCAGTGCATCTGGGAGCACGGGCCCACCAGTCTGCTGGTGTCCATCGGGCAGAA
CCTGGGCGCTCACTGGGGCAGGTATCGCTCTCCGGGGTTCCATGTGCAGTCCTGGTATGA
CGAGGTGAAGGACTACACCTACCCCTACCCGAGCGAGTGCAACCCCTGGTGTCCAGAGAG
GTGCTCGGGGCCTATGTGCACGCACTACACACAGATAGTTTGGGCCACCACCAACAAGAT
CGGTTGTGCTGTGAACACCTGCCGGAAGATGACTGTCTGGGGAGAAGTTTGGGAGAACGC
GGTCTACTTTGTCTGCAATTATTCTCCAAAGGGGAACTGGATTGGAGAAGCCCCCTACAA
GAATGGCCGGCCCTGCTCTGAGTGCCCACCCAGCTATGGAGGCAGCTGCAGGAACAACTT
GTGTTACCGAGAAGAAACCTACACTCCAAAACCTGAAACGGACGAGATGAATGAGGTGGA
AACGGCTCCCATTCCTGAAGAAAACCATGTTTGGCTCCAACCGAGGGTGATGAGACCCAC
CAAGCCCAAGAAAACCTCTGCGGTCAACTACATGACCCAAGTCGTCAGATGTGACACCAA
GATGAAGGACAGGTGCAAAGGGTCCACGTGTAACAGGTACCAGTGCCCAGCAGGCTGCCT
GAACCACAAGGCGAAGATCTTTGGAAGTCTGTTCTATGAAAGCTCGTCTAGCATATGCCG
CGCCGCCATCCACTACGGGATCCTGGATGACAAGGGAGGCCTGGTGGATATCACCAGGAA
CGGGAAGGTCCCCTTCTTCGTGAAGTCTGAGAGACACGGCGTGCAGTCCCTCAGCAAATA
CAAACCTTCCAGCTCATTCATGGTGTCAAAAGTGAAAGTGCAGGATTTGGACTGCTACAC
GACCGTTGCTCAGCTGTGCCCGTTTGAAAAGCCAGCAACTCACTGCCCAAGAATCCATTG
TCCGGCACACTGCAAAGACGAACCTTCCTACTGGGCTCCGGTGTTTGGAACCAACATCTA
TGCAGATACCTCAAGCATCTGCAAGACAGCTGTGCACGCGGGAGTCATCAGCAACGAGAG
TGGGGGTGACGTGGACGTGATGCCCGTGGATAAAAAGAAGACCTACGTGGGCTCGCTCAG
GAATGGAGTTCAGTCTGAAAGCCTGGGGACTCCTCGGGATGGAAAGGCCTTCCGGATCTT
TGCTGTCAGGCATTTCCCTTTGCGGCCGCG**TGA**ATTTCCAGCACCAGGGGAGAAGGGGCG
TCTTCAGGAGGGCTTCGGGGTTTTGCTTTTATTTTTATTTTGTCATTGCGGGGTATATGG
AGAGTCA

FIGURE 4

```
MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLEELLSKYQHNESHSRVRRAIPREDKEEIL
MLHNKLRGQVQPQASNMEYMTWDDELEKSAAAWASQCIWEHGPTSLLVSIGQNLGAHWGR
YRSPGFHVQSWYDEVKDYTYPYPSECNPWCPERCSGPMCTHYTQIVWATTNKIGCAVNTC
RKMTVWGEVWENAVYFVCNYSPKGNWIGEAPYKNGRPCSECPPSYGGSCRNNLCYREETY
TPKPETDEMNEVETAPIPEENHVWLQPRVMRPTKPKKTSAVNYMTQVVRCDTKMKDRCKG
STCNRYQCPAGCLNHKAKIFGSLFYESSSSICRAAIHYGILDDKGGLVDITRNGKVPFFV
KSERHGVQSLSKYKPSSSFMVSKVKVQDLDCYTTVAQLCPFEKPATHCPRIHCPAHCKDE
PSYWAPVFGTNIYADTSSICKTAVHAGVISNESGGDVDVMPVDKKKTYVGSLRNGVQSES
LGTPRDGKAFRIFAVRQ
```

Important features of the protein:

Signal peptide:

1-22

N-glycosylation site:

　　　27-31

　　　41-45

　　451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

　　181-185

　　276-280

　　464-468

Tyrosine kinase phosphorylation site.

　　385-393

N-myristoylation site.

　　111-117

　　115-121

　　174-180

　　204-210

　　227-233

　　300-306

　　447-453

　　470-476

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

　　195-207

SCP-like extracellular protein

　　56-208

FIGURE 5

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGCCTGGATCTTCCA
CC**ATG**TTCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGCATCTCCCTGACTGTCCTCTTCACC
CTCCTTCTCGTTTTCATCATAGTGCCAGCCATTTTTGGAGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAG
TCTGTTAAAAATCTTTGCGTGGGCTACCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACA
AGCCCTACACCAACGGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCGTCGAAGT
GGTAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCCGGAAAGGAAT
GGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTGGAGTCCTGGAACCTGCTGAGCA
GAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCACGGTCCTGTGGGGGTTAGGAGTGCTGATTCGGTAC
TGCTTTCTGCTGCCGCTCAGGATAGCACTGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACTGTGGT
GGGATACTTGCCAAATGGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCG
TGCGAGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCTGTGTGGCC
AATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCCATGGTGGGTCAAGTGCACGG
GGGACTCATGGGTGTGATTCAGAGAGCCATGGTGAAGGCCTGCCCACACGTCTGGTTTGAGCGCTCGGAAGTGA
AGGATCGCCACCTGGTGGCTAAGAGACTGACTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTC
CCAGAAGGAACCTGCATCAATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGT
TTACCCTGTTGCTATCAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAATACGGGATGGTGA
CGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTGCCTCCCATGACTAGAGAG
GCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAAATCTGCCATTGCCAGGCAGGGAGGACTTGTGGACCT
GCTGTGGGATGGGGGCCTGAAGAGGGAGAAGGTGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCA
AGATGATCGTGGGGAACCACAAGGACAGGAGCCGCTCC**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGG
GGTGCCAACGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCCACTGCTGTGTCCTTTCCAGACTCCAGGGCTCC
CCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCGAGCCGCAGCGGGATCCCTGTGCACCCGGCGCAGCCT
ACCCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGACGAGATGCCTTGTTTCTTTTACAATAAG
TCGTTGGAGGAATGCCATTAAAGTGAACTCCCCACCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTG
GCCATGGTCTTGTGCTAGAGATGGCGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGG
CGGCCACCCGCTCTCCAGGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCCAGCCT
TGGAGCTCTGCAGACATGATAGGAAGGAAACTGTCATCTGCAGGGGCTTTCAGCAAAATGAAGGGTTAGATTTT
TATGCTGCTGCTGATGGGGTTACTAAAGGGAGGGGAAGAGGCCAGGTGGGCCGCTGACTGGGCCATGGGGAGAA
CGTGTGTTCGTACTCCAGGCTAACCCTGAACTCCCCATGTGATGCGCGCTTTGTTGAATGTGTGTCTCGGTTTC
CCCATCTGTAATATGAGTCGGGGGGAATGGTGGTGATTCCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCT
GCGGGTGAGTGAAGGACACATCACGTTCAGTGTTTCAAGTACAGGCCCACAAAACGGGGCACGGCAGGCCTGAG
CTCAGAGCTGCTGCACTGGGCTTTGGATTTGTTCTTGTGAGTAAATAAAACTGGCTGGTGAATGA

FIGURE 6

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MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSFGIRKLYMKSLLKIFAWATLRMERGAKEKNHQLYK
PYTNGIIAKDPTSLEEEIKEIRRSGSSKALDNTPEFELSDIFYFCRKGMETIMDDEVTKRFSAEELESWNLLSR
TNYNFQYISLRLTVLWGLGVLIRYCFLLPLRIALAFTGISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICV
RALTAIITYHDRENRPRNGGICVANHTSPIDVIILASDGYYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVK
DRHLVAKRLTEHVQDKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVT
YLLRMMTSWAIVCSVWYLPPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTFKEEQQKLYSK
MIVGNHKDRSRS
```

FIGURE 7A

```
CTCCCTTTCATCTGGTGGCCCTAGCGCCACAAGCTGCCGCTTAGGAAGTCCCTGCCGGGA
GCAGAAGTGGAGACATCAGCAGGATGGCATCGGCAAGTCGCTCCCCTCCCGGGCCTCATC
TGCCAAACGATCATCTCCTCCTCCGAAGTTGTATGCATGACAGGCGAGTGGAAACTTCAC
TAAAATGAAGGCGATTGACACAACAGAAGGAACTCCATCCTTTCGGGGGCTTACGAAAAT
AATAAGTTTAAAAAAAATAGGAAGGGAATTCCCTCGCTCCATGATCACTGAGCGCTCTCC
TAAGGAAAAGGAAATCTCCCGGGGGGTGCCGACTACGGGCGGCGGGCTTAGGATGCTCCC
ACGCTCCCCGACCCCCAATCCCCAGGACCCGCAGGACCTCCGGAGGAACGCCCGCCAGCC
CGCCCGGAGCCACGCGGCACAAGGTGACACGGACCGCGCCGCGCGGGCCCCTCAGCCGCC
TGGGCGAGGCCGGGAGCAGGGAGAGGGGCATCCGCCGGCCCGCGGTACCTTGTACTTATC
AAAGCCAGCCAGCTGCTCCGGGCTCACGTATTCGTAGCCAGCCATGACGACCCGAAAACT
GAGCGCCCACTCGGCAGCGACTCCCGGCTACAAGGCTGTGACACACAAGCACCACACCGG
CTGGGCAAGGATGGCAAAGACTGGGCTGCCCGAGAAGGGACAGAGTCAGGCTGGAGGGGA
ATCTGGATCTGGGCAGCTCCTGGACCAAGAGAATGGAGCAGGGGAATCAGCGCTGGTCTC
CGTCTATGTACATCTGGACTTTCCAGATAAGACCTGGCCCCCTGAACTCTCCAGGACACT
GACTCTCCCTGCTGCCTCAGCTTCCTCTTCCCCAAGGCCTCTTCTCACTGGCCTCAGACT
CACAACAGGTGAGTACATGAGCTGCTTCGAGGCCCAGGGCTTCAAGTGGAACCTGTATGA
GGTGGTGAGGGTGCCCTTGAAGGCGACAGATGTGGCTCGACTTCCATACCAGCTGTCCAT
CTCCTGTGTCACCTCCCCTGGCTTCCAGCTGAGCTGCTGCATCCCCAGCACAAACCTGGC
CTACACCGCGGCCTGGAGCCCTGGAGAGGGCAGCAAAGCTTCCTCCTTCAACGAGTCAGG
CTCTCAGTGCTTTGTGCTGGCTGTTCAGCGCTGCCCGATGGCTGACACCACGTACACTTG
TGACCTGCAGAGCCTGGGCCTGGCTCCACTCAGGGTCCCCATCTCCATCACCATCATCCA
GGATGGAGACATCACCTGCCCTGAGGACGCCTCGGTGCTCACCTGGAATGTCACCAAGGC
TGGCCACGTGGCACAGGCCCCATGTCCTGAGAGCAAGAGGGGCATAGTGAGGAGGCTCTG
TGGGGCTGACGGAGTCTGGGGGCCGGTCCACAGCAGCTGCACAGATGCGAGGCTCCTGGC
CTTGTTCACTAGAACCAAGCTGCTGCAGGCAGGCCAGGGCAGTCCTGCTGAGGAGGTGCC
ACAGATCCTGGCACAGCTGCCAGGGCAGGCGGCAGAGGCAAGTTCACCCTCCGACTTACT
GACCCTGCTGAGCACCATGAAATACGTGGCCAAGGTGGTGGCAGAGGCCAGAATACAGCT
TGACCGCAGAGCCCTGAAGAATCTCCTGATTGCCACAGACAAGGTCCTAGATATGGACAC
CAGGTCTCTGTGGACCCTGGCCCAAGCCCGGAAGCCCTGGGCAGGCTCGACTCTCCTGCT
GGCTGTGGAGACCCTGGCATGCAGCCTGTGCCCACAGGACTACCCCTTCGCCTTCAGCTT
ACCCAATGTGCTGCTGCAGAGCCAGCTGTTTGGACCCACGTTTCCTGCTGACTACAGCAT
CTCCTTCCCTACTCGTCCCCCACTGCAGGCTCAGATTCCCAGGCACTCACTGGCCCCATT
GGTCCGTAATGGAACTGAAATAAGTATTACTAGCCTGGTGCTGCGAAAACTGGACCACCT
TCTGCCCTCAAACTATGGACAAGGGCTGGGGGATTCCCTCTATGCCACTCCTGGCCTGGT
CCTTGTCATTTCCATCATGGCAGGTGACCGGGCCTTCAGCCAGGGAGAGGTCATCATGGA
CTTTGGGAACACAGATGGTTCCCCTCACTGTGTCTTCTGGGATCACAGTCTCTTCCAGGG
CAGGGGGGGTTGGTCCAAAGAAGGGTGCCAGGCACAGGTGGCCAGTGCCAGCCCCACTGC
```

FIGURE 7B

```
TCAGTGCCTCTGCCAGCACCTCACTGCCTTCTCCGTCCTCATGTCCCCACACACTGTTCC
GGAAGAACCCGCTCTGGCGCTGCTGACTCAAGTGGGCTTGGGAGCTTCCATACTGGCGCT
GCTTGTGTGCCTGGGTGTGTACTGGCTGGTGTGGAGAGTCGTGGTGCGGAACAAGATCTC
CTATTTCCGCCACGCCGCCCTGCTCAACATGGTGTTCTGCTTGCTGGCCGCAGACACTTG
CTTCCTGGGCGCCCCATTCCTCTCTCCAGGGCCCCGAAGCCCGCTCTGCCTTGCTGCCGC
CTTCCTCTGTCATTTCCTCTACCTGGCCACCTTTTTCTGGATGCTGGCGCAGGCCCTGGT
GTTGGCCCACCAGCTGCTATTTGTCTTTCACCAGCTGGCAAAGCACCGAGTTCTCCCCCT
CATGGTGCTCCTGGGCTACCTGTGCCCACTGGGGTTGGCAGGTGTCACCCTGGGGCTCTA
CCTACCTCAAGGGCAATACCTGAGGGAGGGGGAATGCTGGTTGGATGGGAAGGGAGGGGC
GTTATACACCTTCGTGGGGCCAGTGCTGGCCATCATAGGCGTGAATGGGCTGGTACTAGC
CATGGCCATGCTGAAGTTGCTGAGACCTTCGCTGTCAGAGGGACCCCCAGCAGAGAAGCG
CCAAGCTCTGCTGGGGGTGATCAAAGCCCTGCTCATTCTTACACCCATCTTTGGCCTCAC
CTGGGGGCTGGGCCTGGCCACTCTGTTAGAGGAAGTCTCCACGGTCCCTCATTACATCTT
CACCATTCTCAACACCCTCCAGGGCGTCTTCATCCTATTGTTTGGTTGCCTCATGGACAG
GAAGATACAAGAAGCTTTGCGCAAACGCTTCTGCCGCGCCCAAGCCCCCAGCTCCACCAT
CTCCCTGGCCACAAATGAAGGCTGCATCTTGGAACACAGCAAAGGAGGAAGCGACACTGC
CAGGAAGACAGATGCTTCAGAGTGAACCACACACGGACCCATGTTCCTGCAAGGGAGTTG
AGGCTGTGTGCTTGAACCCACCAGATGAGCCCTGGCCCAATGCTCTGAACTCTTCCCGCC
TCCCGGAGCTCAGCCCTTGAGAAAGTTATGAAGAAAGGATGACTTACTTGACAGGAACCT
CTGATCTTTCAAACATTGGAGATGAAGGGCAGAATTTGGTTTGTCTTTTCAAGTTTAGGA
AAAGGTGAAGTTAATTGGTCCCTCTTTCTTTAACCTTTAAAAAATCAATATAAAATGTAA
GTTTCTTAACCAT
```

FIGURE 8A

MTTRKLSAHSAATPGYKAVTHKHHTGWARMAKTGLPEKGQSQAGGESGSGQLLDQENGAG
ESALVSVYVHLDFPDKTWPPELSRTLTLPAASASSSPRPLLTGLRLTTGEYMSCFEAQGF
KWNLYEVVRVPLKATDVARLPYQLSISCVTSPGFQLSCCIPSTNLAYTAAWSPGEGSKAS
SFNESGSQCFVLAVQRCPMADTTYTCDLQSLGLAPLRVPISITIIQDGDITCPEDASVLT
WNVTKAGHVAQAPCPESKRGIVRRLCGADGVWGPVHSSCTDARLLALFTRTKLLQAGQGS
PAEEVPQILAQLPGQAAEASSPSDLLTLLSTMKYVAKVVAEARIQLDRRALKNLLIATDK
VLDMDTRSLWTLAQARKPWAGSTLLLAVETLACSLCPQDYPFAFSLPNVLLQSQLFGPTF
PADYSISFPTRPPLQAQIPRHSLAPLVRNGTEISITSLVLRKLDHLLPSNYGQGLGDSLY
ATPGLVLVISIMAGDRAFSQGEVIMDFGNTDGSPHCVFWDHSLFQGRGGWSKEGCQAQVA
SASPTAQCLCQHLTAFSVLMSPHTVPEEPALALLTQVGLGASILALLVCLGVYWLVWRVV
VRNKISYFRHAALLNMVFCLLAADTCFLGAPFLSPGPRSPLCLAAAFLCHFLYLATFFWM
LAQALVLAHQLLFVFHQLAKHRVLPLMVLLGYLCPLGLAGVTLGLYLPQGQYLREGECWL
DGKGGALYTFVGPVLAIIGVNGLVLAMAMLKLLRPSLSEGPPAEKRQALLGVIKALLILT
PIFGLTWGLGLATLLEEVSTVPHYIFTILNTLQGVFILLFGCLMDRKIQEALRKRFCRAQ
APSSTISLATNEGCILEHSKGGSDTARKTDASE

Transmembrane domain:
573-593
609-629
648-668
685-705
728-748
770-790
803-823

N-glycosylation site.
183-186
242-245
449-452

Glycosaminoglycan attachment site.
47-50

cAMP- and cGMP-dependent protein kinase phosphorylation site.
4-7

FIGURE 8B

N-myristoylation site.

39-44

44-49

58-63

103-108

176-181

450-455

472-477

474-479

508-513

512-517

578-583

700-705

725-730

742-747

771-776

784-789

788-793

861-866

862-867

G-protein coupled receptor

231-258

642-671

727-757

771-790

578-597

811-836

7 transmembrane receptor (Secretin family)

568-828

Latrophilin/CL-1-like GPS domain

512-565

FIGURE 9

GGGAACGGAAA**ATG**GCGCCTCACGGCCCGGGTAGTCTTACGACCCTGGTGCCCTGGGCTGCCGCCCTGCTCCTC

GCTCTGGGCGTGGAAAGGGCTCTGGCGCTACCCGAGATATGCACCCAATGTCCAGGGAGCGTGCAAAATTTGTC

AAAAGTGGCCTTTTATTGTAAAACGACACGAGAGCTAATGCTGCATGCCCGTTGCTGCCTGAATCAGAAGGGCA

CCATCTTGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCCTGGTCCAAACTTTCATCAGGCACATACCACT

GTCATCATAGACCTGCAAGCAAACCCCCTCAAAGGTGACTTGGCCAACACCTTCCGTGGCTTTACTCAGCTCCA

GACTCTGATACTGCCACAACATGTCAACTGTCCTGGAGGAATTAATGCCTGGAATACTATCACCTCTTATATAG

ACAACCAAATCTGTCAAGGGCAAAAGAACCTTTGCAATAACACTGGGGACCCAGAAATGTGTCCTGAGAATGGA

TCTTGTGTACCTGATGGTCCAGGTCTTTTGCAGTGTGTTTGTGCTGATGGTTTCCATGGATACAAGTGTATGCG

CCAGGGCTCGTTCTCACTGCTTATGTTCTTCGGGATTCTGGGAGCCACCACTCTATCCGTCTCCATTCTGCTTT

GGGCGACCCAGCGCCGAAAAGCCAAGACTTCA**TGA**ACTACATAGGTCTTACCATTGACCTAAGATCAATCTGAA

CTATCTTAGCCCAGTCAGGGAGCTCTGCTTCCTAGAAAGGCATCTTTCGCCAGTGGATTCGCCTCAAGGTTGAG

GCCGCCATTGGAAGATGAAAAATTGCACTCCCTTGGTGTAGACAAATACCAGTTCCCATTGGTGTTGTTGCCTA

TAATAAACACTTTTTCTTTTTTNAAAAAAAAAAAAAAAAAAAAAA

FIGURE 10

Signal Peptide:

Amino acids 1-30

Transmembrane:

Amino acids 198-212

MAPHGPGSLTTLVPWAAALLLALGVERALALPEICTQCPGSVQNLSKVAFYCKTTRELMLH

ARCCLNQKGTILGLDLQNCSLEDPGPNFHQAHTTVIIDLQANPLKGDLANTFRGFTQLQTL

ILPQHVNCPGGINAWNTITSYIDNQICQGQKNLCNNTGDPEMCPENGSCVPDGPGLLQCVC

ADGFHGYKCMRQGSFSLLMFFGILGATTLSVSILLWATQRRKAKTS

FIGURE 11

```
GCCGCCCCGCCCCGAGACCGGGCCCGGGGGCGCGGGGCGGCGGGATGCGGCGCCCGGGGCG
GCGATGACCGCGGAGCGCACGCCGCGGGCCCGGCCCTGACCCCGCCGCCCGCCCGCTGAGC
CCCCCGCCGAGGTCCGGACAGGCCGGAGATGACGCCGAGCCCCCTGTTGCTGCTCCTGCTGC
CGCCGCTGCTGCTGGGGGGCCTTCCCACCGGCCGGCCGCCGCGCCCGAGGCCCCCCAAAGATGGC
GGACAAGGTGGTCCCACGGCAGGTGGCCCGGCTGGGCCGCACTGTGCGGCTGCAGTGCCCA
GTGGAGGGGGACCCGCCGCCGCTGACCATGTGGACCAAGGATGGCCGCACCATCCACAGCG
GCTGGAGCCGCTTCCGCGTGCTGCCGCAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGA
TGCCGGCGTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACTACACC
CTCGTCGTGCTGGATGACATTAGCCCAGGGAAGGAGAGCCTGGGGCCCGACAGCTCCTCTG
GGGGTCAAGAGGACCCCGCCAGCCAGCAGTGGGCACGACCGCGCTTCACACAGCCCTCCAA
GATGAGGCGCCGGGTGATCGCACGGCCCGTGGGTAGCTCCGTGCGGCTCAAGTGCGTGGCC
AGCGGGCACCCTCGGCCCGACATCACGTGGATGAAGGACGACCAGGCCTTGACGCGCCCAG
AGGCCGCTGAGCCCAGGAAGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGGCCGGAGGA
CAGCGGCAAATACACCTGCCGCGTGTCGAACCGCGCGGGCGCCATCAACGCCACCTACAAG
GTGGATGTGATCCAGCGGACCCGTTCCAAGCCCGTGCTCACAGGCACGCACCCCGTGAACA
CGACGGTGGACTTCGGGGGGACCACGTCCTTCCAGTGCAAGGTGCGCAGCGACGTGAAGCC
GGTGATCCAGTGGCTGAAGCGCGTGGAGTACGGCGCCGAGGGCCGCCACAACTCCACCATC
GATGTGGGCGGCCAGAAGTTTGTGGTGCTGCCCACGGGTGACGTGTGGTCGCGGCCCGACG
GCTCCTACCTCAATAAGCTGCTCATCACCCGTGCCCGCCAGGACGATGCGGGCATGTACAT
CTGCCTTGGCGCCAACACCATGGGCTACAGCTTCCGCAGCGCCTTCCTCACCGTGCTGCCA
GACCCAAAACCGCCAGGGCCACCTGTGGCCTCCTCGTCCTCGGCCACTAGCCTGCCGTGGC
CCGTGGTCATCGGCATCCCAGCCGGCGCTGTCTTCATCCTGGGCACCCTGCTCCTGTGGCT
TTGCCAGGCCCAGAAGAAGCCGTGCACCCCCGCGCCTGCCCCTCCCCTGCCTGGGCACCGC
CCGCCGGGGACGGCCCGCGACCGCAGCGGAGACAAGGACCTTCCCTCGTTGGCCGCCCTCA
GCGCTGGCCCTGGTGTGGGGCTGTGTGAGGAGCATGGGTCTCCGGCAGCCCCCAGCACTT
ACTGGGCCCAGGCCCAGTTGCTGGCCCTAAGTTGTACCCCAAACTCTACACAGACATCCAC
ACACACACACACACACTCTCACACACTCACACGTGGAGGGCAAGGTCCACCAGCACA
TCCACTATCAGTGCTAGACGGCACCGTATCTGCAGTGGGCACGGGGGGGCGGCCAGACAG
GCAGACTGGGAGGATGGAGGACGGACGGCTGCAGACGAAGGCAGGGGACCCATGGCGAGGAGG
AATGGCCAGCACCCCAGGCAGTCGTGTGTGTGAGGCATAGCCCCTGGACACACACACACAGA
CACACACACTACCTGGATGCATGTATGCACACACATGCGCGCACACGTGCTCCCTGAAGGC
ACACGTACGCACACGCACATGCACAGATATGCCGCCTGGGCACACAGATAAGCTGCCCAAA
TGCACGCACACGCACAGAGACATGCCAGAACATACAAGGACATGCTGCCTGAACATACACA
CGCACACCCATGCGCAGATGTGCTGCCTGGACACACACACACACACGGATATGCTGTCTGG
ACGCACACGTGCAGATATGGTATCCGGACACACACGTGCACAGATATGCTGCCTGGACA
CACAGATAATGCTGCCTTGACACACACATGCACGGATATTGCCTGGACACACACACACACA
CACGCGTGCACAGATATGCTGTCTGGACACGCACACACATGCAGATATGCTGCCTGGACAC
ACACTTCCAGACACACGTGCACAGGCGCAGATATGCTGCCTGGACACACGCAGATATGCTG
TCTAGTCACACACACACGCAGACATGCTGTCCGGACACACACACGCATGCACAGATATGCT
GTCCGGACACACACACGCACGCAGATATGCTGCCTGGACACACACACAGATAATGCTGCCT
CAACACTCACACACGTGCAGATATTGCCTGGACACACACGTGCACAGATATGCTGTCTG
GACATGCACACGTGCAGATATGCTGTCCGGATACACACGCACGCACACATGCAGATATG
CTGCCTGGGCACACACTTCCGGACACACATGCACACACAGGTGCAGATATGCTGCCTGGAC
ACACACACAGATAATGCTGCCTCAACACTCACACACGTGCAGATATTGCCTGGACACACAC
ATGTGCACAGATATGCTGTCTGGACATGCACACACGTGCAGATATGCTGTCCGGATACACA
CGCACGCACACATGCAGATATGCTGCCTGGGCACACACTTCCGGACACACATGCACACACA
GGTGCAGATATGCTGCCTGGACACACGCAGACTGACGTGCTTTTGGGAGGGTGTGCCGTGA
AGCCTGCAGTACGTGTGCCGTGAGGCTCATAGTTGATGAGGGACTTTCCCTGCTCCACCGT
CACTCCCCCAACTCTGCCCGCCTCTGTCCCCGCCTCAGTCCCCGCCTCCATCCCCGCCTCT
GTCCCCTGGCCTTGGCGGCTATTTTTGCCACCTGCCTTGGGTGCCCAGGAGTCCCCTACTG
CTGTGGGCTGGGGTTGGGGGCACAGCAGCCCCAAGCCTGAGAGGCTGGAGCCCATGGCTAG
TGGCTCATCCCCAGTGCATTCTCCCCCTGACACAGAGAAGGGGCCTTGGTATTTATATTTA
AGAAATGAAGATAATATTAATAATGATGGAAGGAAGACTGGGTTGCAGGGACTGTGGTCTC
TCCTGGGGCCCGGGACCCGCCTGGTCTTTCAGCCATGCTGATGACCACACCCCGTCCAGGC
CAGACACCACCCCCCACCCCACTGTCGTGGTGGCCCAGATCTCTGTAATTTTATGTAGAG
TTTGAGCTGAAGCCCCGTATATTTAATTTATTTTGTTAAACACAAAA
```

FIGURE 12

MTPSPLLLLLLPPLLLGAFPPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLT
MWTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISP
GKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRPDIT
WMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRS
KPVLTGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVV
LPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVLPDPKPPGPPV
ASSSSATSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRS
GDKDLPSLAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTHSHT
HSHVEGKVHQHIHYQC

FIGURE 13

CGGACGCGTGGGCGTCCGGCGGTCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGG
GCCCCAGCCCACACCTTCACCAGGGCCCAGGAGCCACC**ATG**TGGCGATGTCCACTGGGGCT
ACTGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGC
CGGGAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCC
AGGAGCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGC
CATCTGTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGG
GACTTCTGCCTCGGCGTGCCACCCCCTTTTCCCCGATCCAAGGATGTATGCATGGAGGTC
GTATCTATCCAGTCTTGGGAACGTACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAA
CAGGCAGTGGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTG
GCAGGCTGGGAACCACAGCGCCTTCTGGGGCATGACCCTGGA**TGA**GGGCATTCGCTACCGC
CTGGGCACCATCCGCCCATCTTCCTCGGTCATGAACATGCATGAAATTTATACAGTGCTGA
ACCCAGGGGAGGTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCA
TGAGCCTCTTGACCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCA
TCCGATCGTGTCTCAATCCATTCTCTGGGACACATGACGCCTGTCCTGTCGCCCCAGAACC
TGCTGTCTTGTGACACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTG
GTGGTTCCTGCGTCGCCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAA
CGAGACGAGGCTGGCCCTGCGCCCCCCTGTATGATGCACAGCCGAGCCATGGGTCGGGGCA
AGCGCCAGGCCACTGCCCACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGT
CACTCCTGTCTACCGCCTCGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAAT
GGCCCTGTCCAAGCCCTCATGGAGGTGCATGAGGACTTCTTCCTATACAAGGGAGGCATCT
ACAGCCACACGCCAGTGAGCCTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTC
AGTCAAGATCACAGGATGGGGAGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGG
ACTGCGGCCAACTCCTGGGGCCCAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCG
GCGTCAATGAGTGCGACATCGAGAGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGA
GGACATGGGTCATCACTGAGGCTGCGGGCACCACGCGGGGTCCGGCCTGGGATCCAGGCTA
AGGGCCGGCGGAAGAGGCCCCAATGGGGCGGTGACCCCAGCCTCGCCCGACAGAGCCCGGG
GCGCAGGCGGGCGCCAGGGCGCTAATCCCGGCGCGGGTTCCGCTGACGCAGCGCCCCGCCT
GGGAGCCGCGGGCAGGCGAGACTGGCGGAGCCCCCAGACCTCCCAGTGGGGACGGGGCAGG
GCCTGGCCTGGGAAGAGCACAGCTGCAGATCCCAGGCCTCTGGCGCCCCCACTCAAGACTA
CCAAAGCCAGGACACCTCAAGTCTCCAGCCCCAATACCCCACCCCAATCCCGTATTCTTTT
TTTTTTTTTTTTAGACAGGGTCTTGCTCCGTTGCCCAGGTTGGAGTGCAGTGGCCCATCAG
GGCTCACTGTAACCTCCGACTCCTGGGTTCAAGTGACCCTCCCACCTCAGCCTCTCAAGTA
GCTGGGACTACAGGTGCACCACCACACCTGGCTAATTTTTGTATTTTTTGTAAAGAGGGGG
GTCTCACTGTGTTGCCCAGGCTGGTTTCGAACTCCTGGGCTCAAGCGGTCCACCTGCCTCC
GCCTCCCAAAGTGCTGGGATTGCAGGCATGAGCCACTGCACCCAGCCCTGTATTCTTATTC
TTCAGATATTTATTTTTCTTTTCACTGTTTTAAAATAAAACCAAAGTATTGATAAAAAAAA

FIGURE 14

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQDLCCRGRADD

CALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPIQGCMHGGRIYPVLGTYWDNC

NRCTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300, 411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230, 269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 15

GGCTCAGAGGCCCCACTGGACCCTCGGCTCTTCCTTGGACTTCTTGTGTGTTCTGTGAGCTTCGCTGGATTCAG

GGTCTTGGGCATCAGAGGTGAGAGGGTGGGAAGGTCCGCCGCG**ATG**GGGAAGCCCTGGCTGCGTGCGCTACAGC

TGCTGCTCCTGCTGGGCGCGTCGTGGGCGCGGGCGGGCGCCCGCGCTGCACCTACACCTTCGTGCTGCCCCCG

CAGAAGTTCACGGGCGCTGTGTGCTGGAGCGGCCCCGCATCCACGCGGGCGACGCCCGAGGCCGCCAACGCCAG

CGAGCTGGCGGCGCTGCGCATGCGCGTCGGCCGCCACGAGGAGCTGTTACGCGAGCTGCAGAGGCTGGCGGCGG

CCGACGGCGCCGTGGCCGGCGAGGTGCGCGCGCTGCGCAAGGAGAGCCGCGGCCTGAGCGCGCGCCTGGGCCAG

TTGCGCGCGCAGCTGCAGCACGAGGCGGGGCCCGGGGCGGGCCCGGGGGCGGATCTGGGGGCGGAGCCTGCCGC

GGCGCTGGCGCTGCTCGGGGAGCGCGTGCTCAACGCGTCCGCCGAGGCTCAGCGCGCAGCCGCCCGGTTCCACC

AGCTGGACGTCAAGTTCCGCGAGCTGGCGCAGCTCGTCACCCAGCAGAGCAGTCTCATCGCCCGCCTGGAGCGC

CTGTGCCCGGGAGGCGCGGGCGGGCAGCAGCAGGTCCTGCCGCCACCCCCACTGGTGCCTGTGGTTCCGGTCCG

TCTTGTGGGTAGCACCAGTGACACCAGTAGGATGCTGGACCCAGCCCCAGAGCCCCAGAGAGACCAGACCCAGA

GACAGCAGGAGCCCATGGCTTCTCCCATGCCTGCAGGTCACCCTGCGGTCCCCACCAAGCCTGTGGGCCCGTGG

CAGGATTGTGCAGAGGCCCGCCAGGCAGGCCATGAACAGAGTGGAGTGTATGAACTGCGAGTGGGCCGTCACGT

AGTGTCAGTATGGTGTGAGCAGCAACTGGAGGGTGGAGGCTGGACTGTGATCCAGCGGAGGCAAGATGGTTCAG

TCAACTTCTTCACTACCTGGCAGCACTATAAGGCGGGCTTTGGGCGGCCAGACGGAGAATACTGGCTGGGCCTT

GAACCCGTGTATCAGCTGACCAGCCGTGGGGACCATGAGCTGCTGGTTCTCCTGGAGGACTGGGGGGGCCGTGG

AGCACGTGCCCACTATGATGGCTTCTCCCTGGAACCCGAGAGCGACCACTACCGCCTGCGGCTTGGCCAGTACC

ATGGTGATGCTGGAGACTCTCTTTCCTGGCACAATGACAAGCCCTTCAGCACCGTGGATAGGGACCGAGACTCC

TATTCTGGTAACTGTGCCCTGTACCAGCGGGGAGGCTGGTGGTACCATGCCTGTGCCCACTCCAACCTCAACGG

TGTGTGGCACCACGGCGGCCACTACCGAAGCCGCTACCAGGATGGTGTCTACTGGGCTGAGTTTCGTGGTGGGG

CATATTCTCTCAGGAAGGCCGCCATGCTCATTCGGCCCCTGAAGCTG**TGA**CTCTGTGTTCCTCTGTCCCCTAGG

CCCTAGAGGACATTGGTCAGCAGGAGCCCAAGTTGTTCTGGCCACACCTTCTTTGTGGCTCAGTGCCAATGTGT

CCCACAGAACTTCCCACTGTGGATCTGTGACCCTGGGCGCTGAAAATGGGACCCAGGAATCCCCCCCGTCAATA

TCTTGGCCTCAGATGGCTCCCCAAGGTCATTCATATCTCGGTTTGAGCTCATATCTTATAATAACACAAAGTAG

CCAC

FIGURE 16

Signal sequence: Amino acids 1-20

N-glycosylation sites: Amino acids 58-62;145-149

cAMP- and cGMP-dependent protein kinase phosphorylation site:
                                 Amino acids 97-101

Tyrosine kinase phosphorylation site: Amino acids 441-448

N-myristoylation sites: Amino acids 16-22;23-29;87-93;
                                  108-114;121-127;125-131;129-135;
                                  187-193;293-299;353-359;378-384;
                                  445-451;453-459

Cell attachment sequence: Amino acids 340-343

Fibrinogen beta and gamma chains C-terminal domain signature:
                                 Amino acids 418-431

MGKPWLRALQLLLLLGASWARAGAPRCTYTFVLPPQKFTGAVCWSGPASTRATPEAANASE
LAALRMRVGRHEELLRELQRLAAADGAVAGEVRALRKESRGLSARLGQLRAQLQHEAGPGA
GPGADLGAEPAAALALLGERVLNASAEAQRAAARFHQLDVKFRELAQLVTQQSSLIARLER
LCPGGAGGQQQVLPPPPLVPVVPVRLVGSTSDTSRMLDPAPEPQRDQTQRQQEPMASPMPA
GHPAVPTKPVGPWQDCAEARQAGHEQSGVYELRVGRHVVSVWCEQQLEGGGWTVIQRRQDG
SVNFFTTWQHYKAGFGRPDGEYWLGLEPVYQLTSRGDHELLVLLEDWGGRGARAHYDGFSL
EPESDHYRLRLGQYHGDAGDSLSWHNDKPFSTVDRDRDSYSGNCALYQRGGWWYHACAHSN
LNGVWHHGGHYRSRYQDGVYWAEFRGGAYSLRKAAMLIRPLKL

FIGURE 17

AGCCCACCGAGAGGCGCCTGCAGG**ATG**AAAGCTCTCTGTCTCCTCCTCCTCCCTGTCCTGGGGCTGTTGGTGTC
TAGCAAGACCCTGTGCTCCATGGAAGAAGCCATCAATGAGAGGATCCAGGAGGTCGCCGGCTCCCTAATATTTA
GGGCAATAAGCAGCATTGGCCTGGAGTGCCAGAGCGTCACCTCCAGGGGGGACCTGGCTACTTGCCCCCGAGGC
TTCGCCGTCACCGGCTGCACTTGTGGCTCCGCCTGTGGCTCGTGGGATGTGCGCGCCGAGACCACATGTCACTG
CCAGTGCGCGGGCATGGACTGGACCGGAGCGCGCTGCTGTCGTGTGCAGCCC**TGA**GGTCGCGCGCAGCGCGTGC
ACAGCGCGGGCGGAGGCGGCTCCAGGTCCGGAGGGGTTGCGGGGGAGCTGGAAATAAACCTGGAGATGATGATG
ATGATGATGATGGAAAAA

FIGURE 18

MKALCLLLLPVLGLLVSSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGD
LATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQP

Signal peptide:
1-18

Transmembrane domain:
none

Cell attachment sequence.
57-60

N-myristoylation site.

  13-19
  71-77
  75-81
  95-101
100-106

FIGURE 19A

```
   1  tcagggtcag gtgattctcc cacctcagcc tcctgagtag ctgggagtac aggcacatgc
  61  caccacaccc agataatttt taaatttttt gtagagatgg ggtctcactg tgttgcccag
 121  gctggtctcg agctcctggg ctgaagtgat ccatccacct ccgtccacca aagtgctggg
 181  attacaggtg tgagccaccg tgccctgcct gcatttcttt taatagacat gtctctggat
 241  ggtcaactgg acagttgtgc tcaccctcca catttcctcc cctctactca caccccaagg
 301  tgataatgga ttggcaaccc tgggtgactt aagaattcca tgagcttcat aaatgtcaaa
 361  taagctgtct taccctacta acccctctac catcacaatg atcaaagcaa agccaaatag
 421  cccacacctc tcatcccaca cataccatag tcatcctttc atccatttat ccatccattt
 481  accaacttaa aatattcatt gattacctac tacatatgac actttacttg accaaaattg
 541  gcaaaacaca tagcttaaag ttgtctttct tcctagttag gtggaatgat gcctggtata
 601  tcgtatcatt agaaatggct gaatgaatga gctcactgtt tattaggaga atgagacaca
 661  gaccaaataa ctcaagcata agagagaatg tagttagtgt cctaaaagag atccagagtg
 721  ctgtgtgagt tcaaaggtga gaaagagccc ttctgactga agaaatcagg aaagacttca
 781  tagaagcagt ggtgatatat gagctgactt ctaaaggaca agtaagatta taatagcaga
 841  tatagtaggg gaagggaatt accgaggggg tggcatcaat aaagttttgg gggtaaggaa
 901  gtatgagttc tgggtatgaa aatatgtcta acttggtcag agcataaatt acgtattctg
 961  gaaggtagac tgtgtttgag aacaaatgct agaatacctt aaaagctaat ttgttaggtt
1021  ctgcagagtc agtgatagga cccaagcaga caagtaatta ggaagactaa tttggcaaag
1081  atattataaa atgttggggc tgaacaatta ttacatataa taagagaatt aacaaggtgc
1141  ctgagtgaaa tgtaataaac agaaacaac aaattttgta tgtcaaccaa acctagcagt
1201  caaaaggatt aataacaata agtcatgtag gatactatga attcataaca caaagaaatg
1261  ctaggggaaa tatttgcaat gcttatcaca tccaaaagtt cctttcccta atatacaaag
1321  atctgctaga agtcaacaag ctaaagatca acagctcaat agaaatatgg ccaaacggct
1381  ggacgtggtg gctcatgcct gtaatcccag cattttggga gactgaggca ggattgcttg
1441  agcccaggaa ttcaagacca gcctggtcaa cgtagcgaga ttctgtgtct atattttttaa
1501  aaatttatta aaaaagaaa tacgggcaaa tgagctacct agtctcagaa aagaaaatat
1561  atatgatgtg caactatatt aaaagatttt caatttcact aataattttt tttttttgaga
1621  cagagtcttg ctctgtcgcc aggctggagt gcagtggcac catcttggct cactgcaagc
1681  tctgcctccc gagttcacca ttctcctgcc tcagcctccc aagtagctgg gattacaggc
1741  gcacaccacc acacctggct aatgttttgt attttttagta gaggcggggt ttcaccgtgt
1801  tagccaggat ggcctcgatc tcttgacctc gtgatcagcc caccttggcc tctcaaagtg
1861  ctgtgattac aggcgtgagc caccgcgcct ggccaaattt cactaataat tttaaaaagt
1921  aaattatata tacatgggat atcatgttca cttagattgg cgatgagcag aaagtttgat
1981  aactgtgtca taaacacttg gtaactgtgt tagtgagtgt gtggggagat aggtatcctt
2041  atatgctgct aataggagtg taggctgtaa aattctcatg gtagctagtt tagcaatatc
2101  tataaaaatt acaaatatgc ataactttca gtgagtcaga aattttactt ttaagaattt
```

FIGURE 19B

```
2161 atcttacatg tataatcaca acacgtgtga aatatcgtac acataataga tattggttgc
2221 aatcttttca tagttgtgaa agatgaggaa aaacaatctt aaaagtagtt tggttaaata
2281 aatcatgtca ctcatataca gtgaaatatc atccccattt taaaaagatg atggtggtgg
2341 tgctatacat accgatacag aaagctttct aaaacctttc attaaatgaa aaatgaataa
2401 atcattgcag aacagtgtat atatatctaa aatatctatg gaagaaacca gcaacagcca
2461 ctgctcctgg agaattatgg tcccacacca ctgatcattc tttcagtagg gtgaccatca
2521 tccaaatttg cttgggactg aggggggttcc ttttggtttg aaaaccagga cagtcctagg
2581 aaaagtgaga caagttggtc acatgtcccc aagatgatct tctttcactt atgaacttgc
2641 tactttccca gtcagaatat aaactctgag gggggagact tcctgttttc ttcatgacta
2701 tatctcttgc gcactgtggg gtggaggctg tagaagagga gagaagtaga gaaacagatc
2761 acattgtgtc ttgaagtgtt tcagcaaata tgggcaacac ccttctttta ctagcttgga
2821 accctacctc tgagtgcatt tccctttttta ttatttattt cctgtcagtt ataagagagg
2881 cctaccccctt tgtgagcagt ctaggacttt gtacacctgc taagtaggga gaaggcaggg
2941 gaggtggctg gtttaagggg aacttgaggg aagtagggaa gactcctctc gggacctttg
3001 gagtaggtga cacatgagcc cagccccagc tcacctgcca atccagctga ggagctcacc
3061 tgccaatcca gctgaggctg ggcagaggtg ggtgagaaga gggaaaattg cagggacctc
3121 cagttgggcc aggccagaag ctgctgtagc tttaaccaga cagctcagac ctgtatggag
3181 gctgccagtg acaggttagg tttagggcag agaagaagca agaccatg
```

FIGURE 20

MVGKMWPVLWTLCAVRVTVDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKLLLTHTERVVIWPF

SNKNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMSDLEGNTKSRVRLLVLVPPSKPECGI

EGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQPLAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFC

NITVAVRSPSMNVALYVGIAVGVVAALIIIGIIIYCCCCRGKDDNTEDKEDARPNREAYEEPPEQLRELSRERE

EEDDYRQEEQRSTGRESPDHLDQ

FIGURE 21A

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCCATGCAACCCCGCGCCCTGCGCC

TTAACCAGGACTGCTCCGCGCGCCCCTGAGCCTCGGGCTCCGGCCCGGACCTGCAGCCTCCCAGGTGGCTGGGA

AGAACTCTCCAACAATAAATACATTTGATAAGAAAG**ATG**GCTTTAAAAGTGCTACTAGAACAAGAGAAAACGTT

TTTCACTCTTTTAGTATTACTAGGCTATTTGTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAG

AATTCAGGGATCGGTCTGGAAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGT

GGCTTCGGCTATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTCCA

GAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCAAATTGTTCAGCCACCAGTGATG

CCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAAACTTGTCGGCTTTCAAGACATGGAGTGTGTG

CCTTGTGGAGACCCTCCTCCTCCTTACGAACCGCACTGTGCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCAC

GGCCTCCAGCCCACGGGACACGGCGCTGGCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCCTGCTGGCCCTGC

TCATCCTCTGTGTCATCTATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTCGCAGGAC

ATTCAGTACAACGGCTCTGAGCTGTCGTGTTTTGACAGACCTCAGCTCCACGAATATGCCCACAGAGCCTGCTG

CCAGTGCCGCCGTGACTCAGTGCAGACCTGCGGGCCGGTGCGCTT̲GCTCCCATCCATGTGCTGTGAGGAGGCCT

GCAGCCCCAACCCGGCGACTCTTGGTTGTGGGGTGCATTCTGCAGCCAGTCTTCAGGCAAGAAACGCAGGCCCA

GCCGGGGAGATGGTGCCGACTTTCTTCGGATCCCTCACGCAGTCCATCTGTGGCGAGTTTTCAGATGCCTGGCC

TCTGATGCAGAATCCCATGGGTGGTGACAACATCTCTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACA

TTCATTCTCTCAATCCAGAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGG

GCTGTTCCAGTCCAGTCTCATTCTGAAAACTTTACAGCAGCTACTGATTTATCTAGATATAACAACACACTGGT

AGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAGAGTGGCGCTGTCATCCACC

CAGCCACTCAGACGTCCCTCCAGGAAGCT**TAA**AGAACCTGCTTCTTTCTGCAGTAGAAGCGTGTGCTGGAACCC

AAAGAGTACTCCTTTGTTAGGCTTATGGACTGAGCAGTCTGGACCTTGCATGGCTTCTGGGGCAAAAATAAATC

TGAACCAAACTGACGGCATTTGAAGCCTTTCAGCCAGTTGCTTCTGAGCCAGACCAGCTGTAAGCTGAAACCTC

AATGAATAACAAGAAAAGACTCCAGGCCGACTCATGATACTCTGCATCTTTCCTACATGAGAAGCTTCTCTGCCAC

AAAAGTGACTTCAAAGACTGATGGGTTGAGCTGGCAGCCTATGAGATTGTGGACATATAACAAGAAACAGAAAT

GCCCTCATGCTTATTTTCATGGTGATTGTGGTTTTACAAGACTGAAGACCCAGAGTATACTTTTTCTTTCCAGA

AATAATTTCATACCGCCTATGAAATATCAGATAAATTACCTTAGCTTTTATGTAGAATGGGTTCAAAAGTGAGT

GTTTCTATTTGAGAAGGACACTTTTTCATCATCTAAACTGATTCGCATAGGTGGTTAGAATGGCCCTCATATTG

CCTGCCTAAATCTTGGGTTTATTAGATGAAGTTTACTGAATCAGAGGAATCAGACAGAGGAGGATAGCTCTTTC

CAGAATCCACACTTCTGACCTCAGCCTCGGTCTCATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTAGGG

AATGTGGTCGAGAAAGGGCAGCCCATTGCCCAGAATTAACACATATTGTAGAGACTTGTATGCAAAGGTTGGCA

TATTTATATGAAAATTAGTTGCTATAGAAACATTTGTTGCATCTGTCCCTCTGCCTGAGCTTAGAAGGTTATAG

AAAAAGGGTATTTATAAACATAAATGACCTTTTACTTGCATTGTATCTTATACTAAAGGCTTTAGAAATTACAA

CATATCAGGTTCCCCTACTACTGAAGTAGCCTTCCGTGAGAACACACCACATGTTAGGACTAGAAGAAAATGCA

CAATTTGTAGGGGTTTGGATGAAGCAGCTGTAACTGCCCTAGTGTAGTTTGACCAGGACATTGTCGTGCTCCTT

CCAATTGTGTAAGATTAGTTAGCACATCATCTCCTACTTTAGCCATCCGGTGTTGGATTTAAGAGGACGGTGCT

TCTTTCTATTAAAGTGCTCCATCCCCTACCATCTACACATTAGCATTGTCTCTAGAGCTAAGACAGAAATTAAC

FIGURE 21B

CCCGTTCAGTCACAAAGCAGGGAATGGTTCATTTACTCTTAATCTTTATGCCCTGGAGAAGACCTACTTGAACA

GGGCATATTTTTTAGACTTCTGAACATCAGTATGTTCGAGGGTACTATGATATTTTGGTTTGGAATTGCCCTGC

CCAAGTCACTGTCTTTTAACTTTTAAACTGAATATTAAAATGTATCTGTCTTTCCT

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210

><subunit 1 of 1, 417 aa, 1 stop

><MW: 45305, pI: 5.12, NX(S/T): 6

MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK

ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG

FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT

VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD

SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI

CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV

PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA

FIGURE 23A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGCAGAGGCAGCCTCCTCCAGGAGCGGGGCCC

TGCACACC**ATG**GCCCCCGGGTGGGCAGGGGTCGGCGCCGCCGTGCGCGCCCGCCTGGCGCTGGCCTTGGCGCTG

GCGAGCGTCCTGAGTGGGCCTCCAGCCGTCGCCTGCCCCACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTG

CCACGGGCTGGGCCTCCGCGCGGTTCCTCGGGGCATCCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATA

ATATCACCAGGATCACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGCATCTGGAAGACAACCAG

GTCAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACAAGAATAAGCT

GCAAGTCCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTAGATTTGAGTGAAAACCAGATCC

AGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCGATGTGAAGAACCTGCAACTGGACAACAACCACATCAGC

TGCATTGAAGATGGAGCCTTCCGAGCGCTGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCG

CATCCTGGTCACCAGCTTCAACCACATGCCGAAGATCCGAACTCTGCGCCTCCACTCCAACCACCTCTACTGCG

ACTGCCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCTGCATGGCT

CCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTGTGCCCAGCCCCCCACTCGGA

GCCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTTCGCCCTGCACGTGCAGCAATAACATCGTGGACTGTC

GAGGAAAGGGCTTGATGGAGATTCCTGCCAACTTGCCGGAGGGCATCGTCGAAATACGCCTAGAACAGAACTCC

ATCAAAGCCATCCCTGCAGGAGCCTTCACCCAGTACAAGAAACTGAAGCGAATAGACATCAGCAAGAATCAGAT

ATCGGATATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCCTGTATGGGAACAAGATCA

CCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTCAATGCCAACAAGATCAAC

TGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTTGCTCTCCCTGTATGACAACAAGCTGCAGAC

CATCAGCAAGGGGCTCTTCGCCCCTCTGCAGTCCATCCAGACACTCCACTTAGCCCAAAACCCATTTGTGTGCGG

ACTGCCACTTGAAGTGGCTGGCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCCGCTGCAGCAGC

CCGCGCCGACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGGATTA

CCGCAGCAGGTTCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTCGCTGTGAGGGCACGATTG

TGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCCTGAATATGTCACCGACCTGCGACTGAAT

GACAATGAGGTATCTGTTCTGGAGGCCACTGGCATCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAG

TAACAATAAGATCAAGGAGGTGCGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAG

GGAACCAGCTGGAGACCGTGCACGGGCGCGTGTTCCGTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGAGT

AACTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCGGTGAGACTGCTGTCCCTCTATGACAA

TCGGATCACCACCATCACCCCTGGGGCCTTCACCACGCTTGTCTCCCTGTCCACCATAAACCTCCTGTCCAACC

CCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCAAGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCCT

AGGTGCCAGAAGCCATTTTTTCCTCAAGGAGATTCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGG

CAACGAGGAGAGTAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCGAT

GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTACCTGGAAGGAAAC

CACCTAACAGCCGTGCCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCTTATTGACCTGAGCAACAACAGCAT

CAGCATGCTGACCAATTACACCTTCAGTAACATGTCTCACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGA

GGTGCATCCCCGTCCACGCCTTCAACGGGCTGCGGTCCCTGCGAGTGCTAACCCTCCATGGCAATGACATTTCC

AGCGTTCCTGAAGGCTCCTTCAACGACCTCACATCTCTTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTG

FIGURE 23B

TGACTGCAGTCTTCGGTGGCTGTCGGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCCCGCTGCAGTA
GCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTTCCAGTGCAAAGGGCCAGTGGAC
ATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCCCGTGCAAGAATAACGGGACATGCACCCAGGACCC
TGTGGAGCTGTACCGCTGTGCCTGCCCCTACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCA
TCCAGAACCCCTGTCAGCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCTGC
CCTCTGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAAAACAATGC
CACCTGCGTGGACGGGATCAACAACTACGTGTGTATCTGTCCGCCTAACTACACAGGTGAGCTATGCGACGAGG
TGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTCAGCATGAGGCCAAGTGCATCCCCCTGGACAAAGGATTC
AGCTGCGAGTGTGTCCCTGGCTACAGCGGGAAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCACAAGTG
CCGCCACGGGGCCCAGTGCGTGGACACAATCAATGGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCT
TCTGTGAACACCCCCCACCCATGGTCCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAACGGGGCC
CAGTGCATCGTGGTGCAGCAGGAGCCCACCTGCCGCTGCCCACCAGGCTTCGCCGGCCCCAGATGCGAGAAGCT
CATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAACTGGCCTCCGCCAAGGTCCGACCCCAGGCCAACA
TCTCCCTGCAGGTGGCCACTGACAAGGACAACGGCATCCTTCTCTACAAAGGAGACAATGACCCCCTGGCACTG
GAGCTGTACCAGGGCCACGTGCGGCTGGTCTATGACAGCCTGAGTTCCCCTCCAACCACAGTGTACAGTGTGGA
GACAGTGAATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCTGAACCTAGTAGTGGACA
AAGGAACTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAGCCCCCTCTACCTTGGA
GGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCGCCAGGGCACGGACCGGCCTCTAGGCGGCTTCCACGGATG
CATCCATGAGGTGCGCATCAACAACGAGCTGCAGGACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCAC
CAGGCTGCAAGTCCTGCACCGTGTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAG
TGCCGCCCAGGCTGGACCGGCCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCACCA
TGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGGGGACTTGTGTGACA
ACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCACCATGGGCAGTGCCACATCTCAGACCAAGGG
GAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGCGAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGT
AGTCCGAGAGGTGATCCGCCGCCAGAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAAT
GTCGTGGGGGCTGTGGGCCCCAGTGCTGCCAGCCCACCCGCAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG
GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTCC**TAA**GCCCCTGC
CCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCCATGTGGGACCCCCTGGTGATTCAG
CATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGAAGAGAATATTAAGTATATTGTAAAATAAACAAAAAA
TAGAACTTAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 24A

MAPGWAGVGAAVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPR

NAERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRLNKNKLQ

VLPELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDL

EILTLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMA

PVHLRGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANL

PEGIVEIRLEQNSIKAIPAGAFTQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNK

ITEIAKGLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQ

SIQTLHLAQNPFVCDCHLKWLADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGS

EDYRSRFSSECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVSVLEA

TGIFKKLPNLRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTL

MLRSNLISCVSNDTFAGLSSVRLLSLYDNRITTITPGAFTTLVSLSTINLLSNPFNCNCHL

AWLGKWLRKRRIVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCM

ETVVRCSNKGLRALPRGMPKDVTELYLEGNHLTAVPRELSALRHLTLIDLSNNSISMLTNY

TFSNMSHLSTLILSYNRLRCIPVHAFNGLRSLRVLTLHGNDISSVPEGSFNDLTSLSHLAL

GTNPLHCDCSLRWLSEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFQCKGPVDINIVA

KCNACLSSPCKNNGTCTQDPVELYRCACPYSYKGKDCTVPINTCIQNPCQHGGTCHLSDSH

KDGFSCSCPLGFEGQRCEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDH

CVPELNLCQHEAKCIPLDKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDTINGYTC

TCPQGFSGPFCEHPPPMVLLQTSPCDQYECQNGAQCIVVQQEPTCRCPPGFAGPRCEKLIT

VNFVGKDSYVELASAKVRPQANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSL

SSPPTTVYSVETVNDGQFHSVELVTLNQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGG

IPTSTGLSALRQGTDRPLGGFHGCIHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGL

CRSVEKDSVVCECRPGWTGPLCDQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCD

NKNDSANACSAFKCHHGQCHISDQGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGY

ASCATASKVPIMECRGGCGPQCCQPTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

FIGURE 24B

Signal peptide:

amino acids 1-27

Important features of the protein:

Signal peptide:

Amino acids 1-25

Transmembrane domain:

Amino acids 169-192

N-glycosylation sites:

Amino acids 105-109;214-218;319-323;350-354;368-372;379-383

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 200-204;238-242

Tyrosine kinase phosphorylation site:

Amino acids 207-214

N-myristoylation sites:

Amino acids 55-61;215-221;270-276

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 259-270

TNFR/NGFR family cysteine-rich region proteins:

Amino acids 89-96

FIGURE 25

CAGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGA

GGATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCT

TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT

TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATG

ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA

ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT

CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT

GTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGA

TGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGACAG

AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC

AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG

AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT

CCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA

AATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTA

CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG

GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT

GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA

ATTCCA**TGA**CTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA

CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA

TATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTC

ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA

GAGAATAAAGTGTTCTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 26

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA145887
><subunit 1 of 1, 262 aa, 1 stop
><MW: 30419, pI: 8.44, NX(S/T): 5
MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF
VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT
SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP
NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA
EIYQPMLDRRSQRSEERCVEIP
```

Important features of the protein:
Signal peptide:
Amino Acids   1-20

N-glycosylation sites:
Amino acids   55-59;165-169;170-174;191-195;208-212

N-myristoylation sites:
Amino acids   17-23;20-26;220-226

FIGURE 27

```
GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCCAGACCTGGAGGGTCTCGCTCTGTC
ACACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACCTCCCGGGTTCAAGTGATTCTCATG
CCTCAGCCTCCCGAGTAGCTGGGATTACAGGTGGTGACTTCCAAGAGTGACTCCGTCGGAGGAAAATGACTCCC
CAGTCGCTGCTGCAGACGACACTGTTCCTGCTGAGTCTGCTCTTCCTGGTCCAAGGTGCCCACGGCAGGGGCCA
CAGGGAAGACTTTCGCTTCTGCAGCCAGCGGAACCAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAG
ACCTGCGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCCTTTCCCTGCAGCCCACCCTGCT
TCCCGATCCTTCCCTGACCCCAGGGGCCTCTACCACTTCTGCCTCTACTGGAACCGACATGCTGGGAGATTACA
TCTTCTCTATGGCAAGCGTGACTTCTTGCTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGG
AGAGCCTGGCTCAGGGCCCCCCGCTGTTAGCCACTTCTGTCACCTCCTGGTGGAGCCCTCAGAACATCAGCCTG
CCCAGTGCCGCCAGCTTCACCTTCTCCTTCCACAGTCCTCCCCACACGGCCGCTCACAATGCCTCGGTGGACAT
GTGCGAGCTCAAAAGGGACCTCCAGCTGCTCAGCCAGTTCCTGAAGCATCCCCAGAAGGCCTCAAGGAGGCCCT
CGGCTGCCCCCGCCAGCCAGCAGTTGCAGAGCCTGGAGTCGAAACTGACCTCTGTGAGATTCATGGGGGACATG
GTGTCCTTCGAGGAGGACCGGATCAACGCCACGGTGTGGAAGCTCCAGCCCACAGCCGGCCTCCAGGACCTGCA
CATCCACTCCCGGCAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCC
AGAGGACGAAAGGCCGGAGCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAGCCCTGTTC
CAGGACAAGAATTCCAGCCAAGTCCTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGTAGCCAA
CCTCACGGAGCCCGTGGTGCTCACTTTCCAGCACCAGCTACAGCCGAAGAATGTGACTCTGCAATGTGTGTTCT
GGGTTGAAGACCCCACATTGAGCAGCCCGGGGCATTGGAGCAGTGCTGGGTGTGAGACCGTCAGGAGAGAAACC
CAAACATCCTGCTTCTGCAACCACTTGACCTACTTTGCAGTGCTGATGGTCTCCTCGGTGGAGGTGGACGCCGT
GCACAAGCACTACCTGAGCCTCCTCTCCTACGTGGGCTGTGTCGTCTCTGCCCTGGCCTGCCTTGTCACCATTG
CCGCCTACCTCTGCTCCAGGGTGCCCCTGCCGTGCAGGAGGAAACCTCGGGACTACACCATCAAGGTGCACATG
AACCTGCTGCTGGCCGTCTTCCTGCTGGACACGAGCTTCCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGA
GGCTGGCTGCCGAGCCAGTGCCATCTTCCTGCACTTCTCCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGG
GGTACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCC
ATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACTATGGCCCCATCAT
CTTGGCTGTGTGCATAGGACTCCAGAGGGCGTCATCTACCCTTCCATGTGCTGGATCCGGGACTCCCTGGTCAGCT
ACATCACCAACCTGGGCCTCTTCAGCCTGGTGTTTCTGTTCAACATGGCCATGCTAGCCACCATGGTGGTGCAG
ATCCTGCGGCTGCGCCCCCACACCCAAAAGTGGTCACATGTGCTGACACTGCTGGGCCTCAGCCTGGTCCTTGG
CCTGCCCTGGGCCTTGATCTTCTTCTCCTTTGCTTCTGGCACCTTCCAGCTTGTCGTCCTCTACCTTTTCAGCA
TCATCACCTCCTTCCAAGGCTTCCTCATCTTCATCTGGTACTGGTCCATGCGGCTGCAGGCCGGGGTGGCCCC
TCCCCTCTGAAGAGCAACTCAGACAGCGCCAGGCTCCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGCATCTA
GGCCTCCAGCCCACCTGCCCATGTGATGAAGCAGAGATGCGGCCTCGTCGCACACTGCCTGTGGCCCCCGAGCC
AGGCCCAGCCCCAGGCCAGTCAGCCGCAGACTTTGGAAAGCCCAACGACCATGGAGAGATGGGCCGTTGCCATG
GTGGACGGACTCCCGGGCTGGGCTTTTGAATTGGCCTTGGGGACTACTCGGCTCTCACTCAGCTCCCACGGGAC
TCAGAAGTGCGCCGCCATGCTGCCTAGGGTACTGTCCCCACATCTGTCCCAACCCAGCTGGAGGCCTGGTCTCT
CCTTACAACCCCTGGGCCCAGCCCTCATTGCTGGGGGCCAGGCCTTGGATCTTGAGGGTCTGGCACATCCTTAA
TCCTGTGCCCCTGCCTGGGACAGAAATGTGGCTCCAGTTGCTCTGTCTCTCGTGGTCACCCTGAGGGCACTCTG
CATCCTCTGTCATTTTAACCTCAGGTGGCACCCAGGGCGAATGGGGCCCAGGGCAGACCTTCAGGGCCAGAGCC
CTGGCGGAGGAGAGGCCCTTTGCCAGGAGCACAGCAGCAGCTCGCCTACCTCTGAGCCCAGGCCCCCTCCCTCC
CTCAGCCCCCCAGTCCTCCCTCCATCTTCCCTGGGGTTCTCCTCCTCTCCCAGGGCCTCCTTGCTCCTTCGTTC
ACAGCTGGGGGTCCCCGATTCCAATGCTGTTTTTTGGGGAGTGGTTTCCAGGAGCTGCCTGGTGTCTGCTGTAA
ATGTTTGTCTACTGCACAAGCCTCGGCCTGCCCCTGAGCCAGGCTCGGTACCGATGCGTGGGCTGGGCTAGGTC
CCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTGCTCACCCTGACCAAGCACACGCCTCAGAGGGG
CCCTCAGCCTCTCCTGAAGCCCTCTTGTGGCAAGAACTGTGGACCATGCCAGTCCGTCTGGTTTCCATCCCAC
CACTCCAAGGACTGAGACTGACCTCCTCTGGTGACACTGCCTAGAGCCTGACACTCTCCTAAGAGGTTCTCTC
CAAGCCCCCAAATAGCTCCAGGCGCCCTCGGCCGCCCATCATGGTTAATTCTGTCCAACAAACACACACGGGTA
GATTGCTGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTGGTCACTCCTCCTGCCAACATTCAGTCTG
GTATGTGAGGCGTGCGTGAAGCAAGAACTCCTGGAGCTACAGGGACAGGGAGCCATCATTCCTGCCTGGGAATC
CTGGAAGACTTCCTGCAGGAGTCAGCGTTCAATCTTGACCTTGAAGATGGGAAGGATGTTCTTTTTTACGTACCA
ATTCTTTTGTCTTTTGATATTAAAAAGAAGTACATGTTCATTGTAGAGAATTTGGAAACTGTAGAAGAGAATCA
AGAAGAAAAATAAAAATCAGCTGTTGTAATCGCCTAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
```

FIGURE 28

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921
<subunit 1 of 1, 693 aa, 1 stop
<MW: 77738, pI: 8.87, NX(S/T): 7
```

MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIENS
EEALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCF
QHQEESLAQGPPLLATSVTSWWSPQNISLPSAASFTFSFHSPPHTAAHNASVDMCELKRDL
QLLSQFLKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTA
GLQDLHIHSRQEEEQSEIMEYSVLLPRTLFQRTKGRSGEAEKRLLLVDFSSQALFQDKNSS
QVLGEKVLGIVVQNTKVANLTEPVVLTFQHQLQPKNVTLQCVFWVEDPTLSSPGHWSSAGC
ETVRRETQTSCFCNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVSALACLVTIAAYLC
SRVPLPCRRKPRDYTIKVHMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAIFLHFSLLT
CLSWMGLEGYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAV
HRTPEGVIYPSMCWIRDSLVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVL
TLLGLSLVLGLPWALIFFSFASGTFQLVVLYLFSIITSFQGFLIFIWYWSMRLQARGGPSP
LKSNSDSARLPISSGSTSSSRI

Important features:
Signal peptide:
amino acids 1-25
Putative transmembrane domains:
amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657
Microbodies C-terminal targeting signal.
amino acids 691-693
cAMP- and cGMP-dependent protein kinase phosphorylation sites.
amino acids 198-201 and 370-373
N-glycosylation sites.
amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344
G-protein coupled receptors family 2 proteins
amino acids 475-504

FIGURE 29A

TGTGCAGAATTGTACAGTTGCGAAACCATGTCGCTGGCAGCTGGTGCTGGCGGTGGAGAC

TTCCCTGTGCGGTGCTCAGTGCATCTGCACCCGTGGGGGAGGGAGCTCTTTCTCTGGCCC

TGCAGTCACCTGAGGTTGTTACCATTATGAACGGCCGCTGGGACCCCCGCATGTGCATGT

ACTCCCCCAGAGTGTCCGGGGGCCCCAGCCAAGGGACACATCTCACGCAGCTGGGAACAT

GTGCAGGCTGATGAAGAGAACCGGATGAGGGCTTCACATGAGGAAGCATGTGGCCAGGTC

CTCTCAGAACATCAGCCTCATCTTCCTGTCTCTGATCTATTTCACCAACCACCCCATGTG

TCTCTAGAACCCCAGTGTAGCGAGCTGGAGAGAGGACTGTCCTGAGGGCAGCAGGCCTGG

TTGCAGCTGGCGTGGGGGTCTCAGA**ATG**GAGCCCTCAGCCCTGAGGAAAGCTGGCTCGGA

GCAGGAGGAGGGCTTTGAGGGGCTGCCCAGAAGGGTCACTGACCTGGGGATGGTCTCCAA

TCTCCGGCGCAGCAACAGCAGCCTCTTCAAGAGCTGGAGGCTACAGTGCCCCTTCGGCAA

CAATGACAAGCAAGAAAGCCTCAGTTCGTGGATTCCTGAAAACATCAAGAAGAAAGAATG

CGTGTATTTTGTGGAAAGTTCCAAACTGTCTGATGCTGGGAAGGTGGTGTGTCAGTGTGG

CTACACGCATGAGCAGCACTTGGAGGAGGCTACCAAGCCCCACACCTTCCAGGGCACACA

GTGGGACCCAAAGAAACATGTCCAGGAGATGCCAACCGATGCCTTTGGCGACATCGTCTT

CACGGGCCTGAGCCAGAAGGTGAAAAAGTACGTCCGAGTCTCCCAGGACACGCCCTCCAG

CGTGATCTACCACCTCATGACCCAGCACTGGGGGCTGGACGTCCCCAATCTCTTGATCTC

GGTGACCGGGGGGGCCAAGAACTTCAACATGAAGCCGCGGCTGAAGAGCATTTTCCGCAG

AGGCCTGGTCAAGGTGGCTCAGACCACAGGGGCCTGGATCATCACAGGGGGGTCCCACAC

CGGCGTCATGAAGCAGGTAGGCGAGGCGGTGCGGGACTTCAGCCTGAGCAGCAGCTACAA

GGAAGGCGAGCTCATCACCATCGGAGTCGCCACCTGGGGCACTGTCCACCGCCGCGAGGG

CCTGATCCATCCCACGGGGCAGCTTCCCCGCCGAGTACATACTGGATGAGGATGGCCAAGG

GAACCTGACCTGCCTAGACAGCAACCACTCTCACTTCATCCTCGTGGACGACGGGACCCA

CGGCCAGTACGGGGTGGAGATTCCTCTGAGGACCAGGCTGGAGAAGTTCATATCGGAGCA

GACCAAGGAAAGAGGAGGTGTGTGGCCATCAAGATCCCCATCGTGTGCGTGGTGCTGGAGGG

CGGCCCGGGCACGTTGCACACCATCGACAACGCCACCACCAACGGCACCCCCTGTGTGGT

TGTGGAGGGCTCGGGCCGCGTGGCCGACGTCATTGCCCAGGTGGCCAACCTGCCTGTCTC

GGACATCACTATCTCCCTGATCCAGCAGAAACTGAGCGTGTTCTTCCAGGAGATGTTTGA

GACCTTCACGGAAAGCAGGATTGTCGAGTGGACCAAAAAGATCCAAGATATTGTCCGGAG

GCGGCAGCTGCTGACTGTCTTCCGGGAAGGCAAGGATGGTCAGCAGGACGTGGATGTGGC

CATCTTGCAGGCCTTGCTGAAAGCCTCACGGAGCCAAGACCACTTTGGCCACGAGAACTG

GGACCACCAGCTGAAACTGGCAGTGGCATGGAATCGCGTGGACATTGCCCGCAGTGAGAT

CTTCATGGATGAGTGGCAGTGGAAGCCTTCAGATCTGCACCCCACGATGACAGCTGCACT

CATCTCCAACAAGCCTGAGTTTGTGAAGCTCTTCCTGGAAAACGGGGTGCAGCTGAAGGA

GTTTGTCACCTGGGACACCTTGCTCTACCTGTACGAGAACCTGGACCCCTCCTGCCTGTT

CCACAGCAAGCTGCAAAAGGTGCTGGTGGAGGATCCCGAGCGCCCGGCTTGCGCGCCCGC

GGCGCCCGCCTGCAGATGCACCACGTGGCCCAGGTGCTGCGGGAGCTGCTGGGGGACTT

FIGURE 29B

```
CACGCAGCCGCTTTATCCCCGGCCCCGGCACAACGACCGGCTGCGGCTCCTGCTGCCCGT
TCCCCACGTCAAGCTCAACGTGCAGGGAGTGAGCCTCCGGTCCCTCTACAAGCGTTCCTC
AGGCCATGTGACCTTCACCATGGACCCCATCCGTGACCTTCTCATTTGGGCCATTGTCCA
GAACCGTCGGGAGCTGGCAGGAATCATCTGGGCTCAGAGCCAGGACTGCATCGCAGCGGC
CTTGGCCTGCAGCAAGATCCTGAAGGAACTGTCCAAGGAGGAGGAGGACACGGACAGCTC
GGAGGAGATGCTGGCGCTGGCGGAGGAGTATGAGCACAGAGCCATCGGGGTCTTCACCGA
GTGCTACCGGAAGGACGAAGAGAGAGCCCAGAAACTGCTCACCCGCGTGTCCGAGGCCTG
GGGGAAGACCACCTGCCTGCAGCTCGCCCTGGAGGCCAAGGACATGAAGTTTGTGTCTCA
CGGGGGCATCCAGGCCTTCCTGACCAAGGTGTGGTGGGGCCAGCTCTCCGTGGACAATGG
GCTGTGGCGTGTGACCCTGTGCATGCTGGCCTTCCCGCTGCTCCTCACCGGCCTCATCTC
CTTCAGGGAGAAGAGGCTGCAGGATGTGGGCACCCCCGCGGCCCGCGCCCGTGCCTTCTT
CACCGCACCCGTGGTGGTCTTCCACCTGAACATCCTCTCCTACTTCGCCTTCCTCTGCCT
GTTCGCCTACGTGCTCATGGTGGACTTCCAGCCTGTGCCCTCCTGGTGCGAGTGTGCCAT
CTACCTCTGGCTCTTCTCCTTGGTGTGCGAGGAGATGCGGCAGCTCTTCTATGACCCTGA
CGAGTGCGGGCTGATGAAGAAGGCAGCCTTGTACTTCAGTGACTTCTGGAATAAGCTGGA
CGTCGGCGCAATCTTGCTCTTCGTGGCAGGGCTGACCTGCAGGCTCATCCCGGCGACGCT
GTACCCCGGGCGCGTCATCCTCTCTCTGGACTTCATCCTGTTCTGCCTCCGGCTCATGCA
CATTTTTACCATCAGTAAGACGCTGGGGCCCAAGATCATCATTGTGAAGCGGATGATGAA
GGACGTCTTCTTCTTCCTCTTCCTGCTGGCTGTGTGGGTGGTGTCCTTCGGGGTGGCCAA
GCAGGCCATCCTCATCCACAACGAGCGCCGGGTGGACTGGCTGTTCCGAGGGGCCGTCTA
CCACTCCTACCTCACCATCTTCGGGCAGATCCCGGGCTACATCGACGGTGTGAACTTCAA
CCCGGAGCACTGCAGCCCCAATGGCACCGACCCCTACAAGCCTAAGTGCCCCGAGAGCGA
CGCGACGCAGCAGAGGCCGGCCTTCCCTGAGTGGCTGACGGTCCTCCTACTCTGCCTCTA
CCTGCTCTTCACCAACATCCTGCTGCTCAACCTCCTCATCGCCATGTTCAACTACACCTT
CCAGCAGGTGCAGGAGCACACGGACCAGATTTGGAAGTTCCAGCGCCATGACCTGATCGA
GGAGTACCACGGCCGCCCCGCCGCGCCGCCCCCCTTCATCCTCCTCAGCCACCTGCAGCT
CTTCATCAAGAGGGTGGTCCTGAAGACTCCGGCCAAGAGGCACAAGCAGCTCAAGAACAA
GCTGGAGAAGAACGAGGAGGCGGCCCTGCTATCCTGGGAGATCTACCTGAAGGAGAACTA
CCTCCAGAACCGACAGTTCCAGCAAAAGCAGCGGCCCGAGCAGAAGATCGAGGACATCAG
CAATAAGGTTGACGCCATGGTGGACCTGCTGGACCTGGACCCACTGAAGAGGTCGGGCTC
CATGGAGCAGAGGTTGGCCTCCCTGGAGGAGCAGGTGGCCCAGACAGCCCGAGCCCTGCA
CTGGATCGTGAGGACGCTGCGGGCCAGCGGCTTCAGCTCGGAGGCGGACGTCCCCACTCT
GGCCTCCCAGAAGGCCGCGGAGGAGCCGGATGCTGAGCCGGGAGGCAGGAAGAAGACGGA
GGAGCCGGGCGACAGCTACCACGTGAATGCCCGGCACCTCCTCTACCCCAACTGCCCTGT
CACGCGCTTCCCCGTGCCCAACGAGAAGGTGCCCTGGGAGACGGAGTTCCTGATCTATGA
```

FIGURE 29C

CCCACCCTTTTTACACGGCAGAGAGGAAGGACGCGGCCGCCATGGACCCCATGGGAGACAC
CCTGGAGCCACTGTCCACGATCCAGTACAACGTGGTGGATGGCCTGAGGGACCGCCGGAG
CTTCCACGGGCCGTACACAGTGCAGGCCGGGTTGCCCCTGAACCCCATGGGCCGCACAGG
ACTGCGTGGGCGCGGGAGCCTCAGCTGCTTCGGACCCAACCACACGCTGTACCCCATGGT
CACGCGGTGGAGGCGGAACGAGGATGGAGCCATCTGCAGGAAGAGCATAAAGAAGATGCT
GGAAGTGCTGGTGGTGAAGCTCCCTCTCTCCGAGCACTGGGCCCTGCCTGGGGGCTCCCG
GGAGCCAGGGGAGATGCTACCTCGGAAGCTGAAGCGGATCCTCCGGCAGGAGCACTGGCC
GTCTTTTGAAAACTTGCTGAAGTGCGGCATGGAGGTGTACAAAGGCTACATGGATGACCC
GAGGAACACGGACAATGCCTGGATCGAGACGGTGGCCGTCAGCGTCCACTTCCAGGACCA
GAATGACGTGGAGCTGAACAGGCTGAACTCTAACCTGCACGCCTGCGACTCGGGGGCCTC
CATCCGATGGCAGGTGGTGGACAGGCGCATCCCACTCTATGCGAACCACAAGACCCTCCT
CCAGAAGGCAGCCGCTGAGTTCGGGGCTCACTAC**TGA**CTGTGCCCTCAGGCTGGGCGGCT
CCAGTCCATAGACGTTCCCCCCAGAAACCAGGGCTTCTCTCTCCTGAGCCTGGCCAGGAC
TCAGGCTGTTCCTGGGCCCTGCACATGATGGGGTTTGGTGGACCCAGTGCCCCTCACGGC
TGCCGCAAGTCTGCTGCAGATGACCTCATGAACTGGAAGGGGTCAAGGTGACCCGGGAGG
AGAGCTCAAGACAGGGCACAGGCTACTCAGAGCTGAGGGGCCCCTGGGACCCTTGGCCAT
CAGGCGAGGGGCTGGGCCTGTGCAGCTGGGCCCTTGGCCAGAGTCCACTCCCTTCCTGGC
TGTGTCACCCCGAGCAGCTCATCCACCATGGAGGTCATTGGCCTGAGGCAAGTTCCCCGG
AGAGTCGGGATCCCCTGTGGCCCCCTCAGGCCTATGTCTGTGAGGAAGGGGCCCTGCCAC
TCTCCCCAAGAGGGCCTCCATGTTTCGAGGTGCCTCAACATGGAGCCTTGCCTGGCCTGG
GCTAGGGGCACTGTCTGAACTCCTGACTGTCAGGATAAACTCCGTGGGGGTACAGGAGCC
CAGACAAAGCCCAGGCCTGTCAAGAGACGCAGAGGGCCCCTGCCAGGGTTGGCCCCAGGG
ACCCTGGGACGAGGCTGCAGAAGCTCTCCCTCCCTACTCCCTGGGAGCCACGTGCTGGCC
ATGTGGCCAGGGACGGCATGAGCAGGAGGCGGGGACGTGGGGCCTTCTGGTTTGGTGTC
AACAGCTCACAGGAGCGTGAACCATGAGGGCCCTCAGGAGGGGAACGTGGTAAAACCCAA
GACATTAAATCTGCCATCTCAGGCCTGGCTGGCTCTTCTGTGCTTTCCACAAATAAAGTT
CCTGACACGTCCAGGGCCAGGGGCTGTGTGACGGCTGCCTGAAGTTCTCCTCGATCCCCC
GGTGAGCTTCCTGCAGCCTGTGGATGTCCTGCAGCCCCTCAGCCCTACCCCCAAGTTTCT
CCTCTGACCCATCAGCTCCCTGTCTTCATTTTCCTAAACCTGGGCTCCAGCATCGTCCCC
AAGCCCACCAGGCCAGGATGCAGGCATCCACATGCCCTCCTCCTTGGCTTCCCCTGCGTG
GTGGTGCCAATGTGCCCTGGCACCCCTGCAGAGGCTCCGGATGGAGCCTGGGGCTGCCTG
GCCACTGAGCACTGGCCGAGGTGATGCCCACCCTTCCCTGGACAGGCCTCTGTCTTCCAC
CTGACCCAAAGCTCTCTAGCCACCCCCTTGTCCCCAGTAT

FIGURE 30

```
><DNA226659 [min]
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA226659
><subunit 1 of 1, 1503 aa, 1 stop
><MW: 171226, pI: 7.73, NX(S/T): 8


MEPSALRKAGSEQEEGFEGLPRRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS
SWIPENIKKKECVYFVESSKLSDAGKVVCQCGYTHEQHLEEATKPHTFQGTQWDPKKHVQ
EMPTDAFGDIVFTGLSQKVKKYVRVSQDTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNF
NMKPRLKSIFRRGLVKVAQTTGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG
VATWGTVHRREGLIHPTGSFPAEYILDEDGQGNLTCLDSNHSHFILVDDGTHGQYGVEIP
LRTRLEKFISEQTKERGGVAIKIPIVCVVLEGGPGTLHTIDNATTNGTPCVVVEGSGRVA
DVIAQVANLPVSDITISLIQQKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR
EGKDGQQDVDVAILQALLKASRSQDHFGHENWDHQLKLAVAWNRVDIARSEIFMDEWQWK
PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLDPSCLFHSKLQKVL
VEDPERPACAPAAPRLQMHHVAQVLRELLGDFTQPLYPRPRHNDRLRLLLPVPHVKLNVQ
GVSLRSLYKRSSGHVTFTMDPIRDLLIWAIVQNRRELAGIIWAQSQDCIAAALACSKILK
ELSKEEEDTDSSEEMLALAEEYEHRAIGVFTECYRKDEERAQKLLTRVSEAWGKTTCLQL
ALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTLCMLAFPLLLTGLISFREKRLQD
VGTPAARARAFFTAPVVVFHLNILSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFSLV
CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS
LDFILFCLRLMHIFTISKTLGPKIIIVKRMMKDVFFFLFLLAVWVVSFGVAKQAILIHNE
RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFPEHCSPNGTDPYKPKCPESDATQQRPAF
PEWLTVLLLCLYLLFTNILLLNLLIAMFNYTFQQVQEHTDQIWKFQRHDLIEEYHGRPAA
PPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEKNEEAALLSWEIYLKENYLQNRQFQQ
KQRPEQKIEDISNKVDAMVDLLDLDPLKRSGSMEQRLASLEEQVAQTARALHWIVRTLRA
SGFSSEADVPTLASQKAAEEPDAEPGGRKKTEEPGDSYHVNARHLLYPNCPVTRFPVPNE
KVPWETEFLIYDPPFYTAERKDAAAMDPMGDTLEPLSTIQYNVVDGLRDRRSFHGPYTVQ
AGLPLNPMGRTGLRGRGSLSCFGPNHTLYPMVTRWRRNEDGAICRKSIKKMLEVLVVKLP
LSEHWALPGGSREPGEMLPRKLKRILRQEHWPSFENLLKCGMEVYKGYMDDPRNTDNAWI
ETVAVSVHFQDQNDVELNRLNSNLHACDSGASIRWQVVDRRIPLYANHKTLLQKAAAEFG
AHY
```

FIGURE 31

```
GATGGCGCAGCCACAGCTTCTGTGAGATTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGACCAGAAGGG
TGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAAACAAGTTTTGACATTTCCCCTG
AAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAG
CCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGA
AATCTTCTCTTCACGGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAG**ATG**AAAG
CCTCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACA
CTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAG
TGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACAAAGCCTG
CGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCT
GACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTC
TCATGCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAA
AGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAGGAGACA
GAA**TAG**GAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGA
GGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTA
CTTGCTTCCTTGCATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAA
TATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTT
TTACTTGGACATGAAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTT
ATACAGTAAAAAAAAAAAACCTTGTAAATTCTAGAAGAGTGGCTAGGGGGGTTATTCATTTGTATTCAACTAAG
GACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGA
ATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAA
TTGTGTATCTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAA
AAAAAAAAAAAAAAAA
```

FIGURE 32

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500

><subunit 1 of 1, 176 aa, 1 stop

><MW: 20056, pI: 9.13, NX(S/T): 0

MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSEIRGSVQAKDGNI

DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK

KDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE